

REPLACEMENT SHEET

BssHII **SpeI**
 1 GCGCGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCA
 57 TTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCC
 113 GCCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTT
 169 CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGG
NdeI
 225 TAAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT
CMV promotor
 281 TGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTAT
SnaBI
 337 GGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTG
 393 ATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATT
 449 TCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAATCAAC
 505 GGGACTTTCCAAAATGTCGTAACAACCTCCGCCCATTTGACGCAAATGGGCGGTAGG
SacI
 561 CGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCAC
T7 promotor **HindIII** **XbaI**
 617 TGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTTGGT
SfiI
AgeI **NotI**
 673 ACCGGTGCGATGGCACCCCTGCATGCTGCTCCTGCTGTTGGCGGCCCGCCCTGGCCCC
 1▶MetAlaProCysMetLeuLeuLeuLeuLeuAlaAlaAlaLeuAlaPro
ApaI
EcoO109I **AvaI**
 729 GACTCAGACCCGCGCGGGGGCCCAAAAGCCCGAGGTGATCGATGCCAGCGAGCTGA
 16▶oThrGlnThrArgAlaGlyAlaGlnLysProGluValIleAspAlaSerGluLeuT
 785 CCCCCGCGTGACCACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAG
 35▶hrProAlaValThrThrTyrLysLeuValIleAsnGlyLysThrLeuLysGlyGlu
SacI
 841 ACCACCACCGAGGCCGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGC
 54▶ThrThrThrGluAlaValAspAlaAlaThrAlaGluLysValPheLysGlnTyrAl
 897 TAATGACAACGGGTCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCA
 72▶aAsnAspAsnGlyValAspGlyGluTrpThrTyrAspAspAlaThrLysThrPheT
AvaI
2x Protein G
 953 CCGTGACCGAGAAAGCCCGAGGTGATCGATGCCAGCGAGCTGACCCCCGCGGTGACC
 91▶hrValThrGluLysProGluValIleAspAlaSerGluLeuThrProAlaValThr
 1009 ACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAGACCACCAACCGAGGC
 110▶ThrTyrLysLeuValIleAsnGlyLysThrLeuLysGlyGluThrThrThrGluAl
SacI
 1065 CGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGCTAATGACAACGGGG
 128▶aValAspAlaAlaThrAlaGluLysValPheLysGlnTyrAlaAsnAspAsnGlyV

Figure 3B (cont'd I)

REPLACEMENT SHEET

1121 TCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCACCGTGACCGAGGCG
 147▶ a l Asp Gl y Gl u Tr p Thr Tyr Asp Asp Al a Thr Lys Thr Phe Thr Val Thr Gl u Al a
 1177 GCCGCAGAACAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGTCGACGAACA
 166▶ Al a Al a Gl u Gl n Lys Leu l l e Ser Gl u Gl u Asp Leu Asn Gl y Al a Val Asp Gl u Gl
 1233 AAACTCATCTCAGAAGAGGATCTGAATGCTGTGGGCCAGGACACGCAGGAGGTCA
 184▶ n Lys Leu l l e Ser Gl u Gl u Asp Leu Asn Al a Val Gl y Gl n Asp Thr Gl n Gl u Val l
 1289 TCGTGGTGCCCACTCCTTGCCCTTTAAGGTGGTGGTGATCTCAGCCATCCTGGCC
 203▶ l e Val Val Pro Hl s Ser Leu Pro Phe Lys Val Val Val l l e Ser Al a l l e Leu Al a
 1345 CTGGTGGTGCTCACCATCATCTCCCTTATCATCTCATGCTTTGGCAGAAGAA
 222▶ Leu Val Val Leu Thr l l e l l e Ser Leu l l e l l e Leu l l e Met Leu Tr p Gl n Lys Ly
 1401 GCCACGTTCTGTCGGCCGATCGAGAATCCATCTAGAGCTATTCTATAGTGTCACCTA
 240▶ s Pr o Arg Ser Ser Al a Asp Arg Gl u Ser l l e e e e
 1457 AATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT
 1513 TGT TTGCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTCTC
 1569 TTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCA TTCTATT
 1625 CTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
 1681 GCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACAGTGGCG
 1737 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA
 1793 AGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA
 1849 GGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGA
 1905 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG
 1961 CTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGG
 2017 GAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTCT
 2073 GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGC
 2129 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC
 2185 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA
 2241 GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTAT
 2297 CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCG
 2353 GCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACG
 2409 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC

Figure 3B (cont'd II)

REPLACEMENT SHEET

2465 TCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGA
 2521 TCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATA
 EcoO109I
 Bsu36I AlwNI
 2577 TATGAGTAACCTGAGGCTATGGCAGGGCCTGCCGCCCCGACGTTGGCTGCGAGCCC
 2633 TGGGCGCTTCACCCGAACTTGGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGT
 2689 ATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGA
 TK poly A
 2745 ACCCCGCGTTTATGAACAAACGACCCAACACCGTGCGTTTTATTCTGTCTTTTTAT
 2801 TGCCGTCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTTAGCC
 AvrII
 2857 TCCCCCTAGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATC
 2913 CAGCCGGCGTCCCCGAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGT
 BstBI
 2969 GGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTGGTCATTTCGAACC
 3025 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCG
 2634 ***PhePheGluAspLeuLeuArgTyrPheAlaIleArgGlnSer
 3081 AATCGGGAGCGGCGATACCGTAAAGCAGGGAAGCGGTGAGCCCATTCGCCGCCA
 2484 rAspProAlaAlaIleGlyTyrLeuValLeuPheArgAspAlaTrpGluGlyGlyL
 SspI RsrII
 3137 AGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCAC
 2294 euGluGluAlaIleAspArgThrAlaLeuAlaIleAspGlnTyrArgAspAlaVal
 3193 ACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTCCACCATGATAT
 2114 GlyLeuArgGlyCysAspIlePheGlySerPheArgGlyAsnGluValMetIleAs
 3249 TCGGCAAGCAGGCATCGCCATGGGTACGACGAGATCCTCGCCGTGCGGCATGCTC
 1924 nProLeuCysAlaAspGlyHisThrValValLeuAspGluGlyAspProMetSerA
 3305 GCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTGATCATC
 1734 IalysLeuArgAlaPheLeuGluAlaProAlaLeuGlyGlnHisGluGlnAspAsp
 3361 CTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCG
 1554 GlnAspValLeuGlyAlaGluMetArgThrArgAlaArgGluIleArgHisLysAl
 3417 CTTGGTGGTGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCA
 1364 aGlnHisAspPheProCysThrAlaProAspLeuThrHisLeuArgArgMetAla
 3473 TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG
 1174 spAlaMetIleSerValLysGluAlaProAlaLeuHisSerSerLeuLeuAspGln
 Tth111I
 3529 CCCCCGCACTTCGCCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTGGA
 994 GlyProValGluGlyLeuLeuLeuTrpAspArgGlyAlaGluThrValValAspLe
 Neo-R.
 PvuIIFspI MscI
 3585 GCACAGCTGCGCAAGGAACGCCCGTCTGGCCAGCCACGATAGCCGCGCTGCCTCG
 804 uValAlaAlaCysProValGlyThrThrAlaLeuTrpSerLeuArgAlaAlaGlu
 NarI
 3641 TCTTGCAAGTTCATTCAGGGCACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCG
 614 spGlnLeuGluAsnLeuAlaGlySerLeuAspThrLysValPheLeuValProArg
 3697 CCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTG
 434 GlyGlnAlaSerLeuArgPheValAlaAlaAspSerCysGlyIleThrGlnGlnAl
 3753 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAAT
 244 aTrpAspTyrGlyPheLeuArgGluValTrpAlaAlaProSerGlyAlaHisLeuG
 BsaBI
 3809 CCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTGC
 54 IlyAspGlnGluIleMet
 StuI
 AvrII BseRI
 3865 AAAAGCCTAGGCCTCCAAAAAGCCTCCTCACTACTTCTGGAATAGCTCAGAGGCC

Figure 3B (cont'd III)

REPLACEMENT SHEET

BseRI
 3921 GAGGAGGGCGGCCTCGGCCTCTGCATAAATAAAAAAATTAGTCAGCCATGGGGCGG

3977 AGAATGGGCGGAAGTGGGCGGAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGA
 SV40 ori & Promotor

4033 CTATGGTTGCTGACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAG
 NsiI

4089 CCTGGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGCATACT
 SexAI NsiI

4145 TCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGACACACATTCCACA
 PvuII

4201 GCTGGTTCTTTCCGCCTCAGGACTCTTCTTTTTCAATAAAJCAATCTAAAGTATA
 Bsu36I

4257 TATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC
 2874 ==Tr pHI aLysI l eLeuSerAl aGlyI l eGI u
 Eam1105I

4313 AGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAA
 2764 Al aI l eGI nAr gAsnAr gGI uAspMetThrAl aGI nSer GI yThr Thr Tyr I l eVa
 4369 CTACGATACGGGAGGGCTTACCATTCTGGCCCCAGTGCTGCAATGATACCGCGAGAC
 2574 l Va l l eAr gSer Pr oLysGI yAspPr oGI yLeuAl aAl a l l eGI yAr gSer G
 4425 CCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGGGCCGA
 2384 l yAr gGI uGI yAl aGI ySer LysAspAl a l l ePheTrpGI yAl aPr oLeuAl aSer
 4481 GCGCAGAAAGTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCC
 2204 Ar gLeuLeuPr oGI yAl aVal LysAspAl aGI uMetTr pAspI l eLeuGI nGI nAr
 FspI Psp1406I

4537 GCGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATT
 2014 gSerAl aLeuThr LeuLeuGI uGI yThr LeuLeuLysAr gLeuThr ThrAl aMe tA
 4593 GCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTACAGCTCCGG
 1824 l aVal Pr oMetThr ThrAspAr gGI uAspAsnPr o l l eAl aGI uAsnLeuGI uPr o
 4649 TTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTA
 1644 GI uTr pAr gAspLeuAr gThr Val l eAspGI yMetAsnHl sLeuPheAl aThr Le
 PvuII

4705 GCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCACTGTTATCACTC
 1454 uGI uLysPr oGI yGI y l l eThr Thr LeuLeuLeuAsnAl aAl aThr AsnAspSerM
 bla

4761 ATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTT
 1264 etThr l l eAl aAl aSer CysLeuGI uAr gVal ThrMetGI yAspThr LeuHl sLys
 Scal

4817 TTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGAC
 1084 GI uThr Val Pr oSerTyr GI uVal l eLeuAspAsnGI nSerTyrHl s l l eAr gAr gGI
 4873 CGAGTTGCTCTTGGCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACT
 894 yLeuGI nGI uGI nGI yAl aAspI l eAr gSer LeuVal Al aGI yCysLeuLeuVal L
 Psp1406I

4929 TTAAAAGTGCTCATCATTGGAACGTTCTTCTGGGGCGAAAACCTCTCAAGGATCTT
 704 ysPheThr SerMetMetPr oPheAr gGI uGI uPr oAr gPheSer GI uLeu l l eLys
 ApaLI

4985 ACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCCACTGATCTTCAG
 524 GI ySerAsnLeuAspLeuGI u l l eTyr GI yVal Ar gAl aGI yLeuGI nAspGI uAl
 5041 CATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCC
 334 aAspLysVal l eLysVal l eLeuThr GI uPr oHl sAl aPheVal Pr oLeuCysPheAl aA
 5097 GCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCTTTT
 144 l aPhePhePr o l l eLeuAl aVal Ar gPheHl sGI n l l eSerMet
 SspI BspHI

5153 TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG
 5209 AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG
 5265 CCACCTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGGCGGGTGTGGTGGTTACGCG

Figure 3B (cont'd IV)

REPLACEMENT SHEET

Stem loop A
 5321 CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCC
 5377 CTTCCTTTCTCGCCACGTTGCGCCGGCTT7CCCCGTCAAGCTCTAAATCGGGGGCTC
 f1 IR Stem loop B
 5433 CCTTTAGGGTTCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTA
 DrIII Stem loop C Primer-RNA
 5489 GGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGA
 Start Transcription
 VS-Synthese Nicking site Stem loop D Stem loop E
 5545 CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTC
 5601 AACCTATCTCGGTCTATTCTTTTGATTATAAGGGATTTTGCCGATTTCGGCCTA
 Apol Apol SspI
 5657 TTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATAT
 5713 TAACGCTTACAATTTAC

Figure 3B (cont'd V)